Redox Proteomics: From Protein Modifications to Cellular Dysfunction and Diseases

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Oxidative stress features in important biological scenarios such as the etiology of disease (e.g., Alzheimer's Disease), toxicology, aging, and signal transduction. It can result in structural alterations of biomolecules which, in turn, can disrupt biological function. More than 70% of reactive oxygen species are absorbed by proteins, resulting in a wide variety of structural modifications. Thus, oxidative stress has the potential to introduce extensive complexity into the proteome, and redox proteomics focuses on using proteomics methods to elucidate redox-modulated changes to the proteome. Such studies can include looking at changes in levels of specific proteins within the proteome or probing post-translational redox-based changes in protein structure. Mass spectrometry has obvious and fundamental relevance to these studies.

This book is divided logically into three parts: oxidatively modified proteins and proteomic technologies; cellular aspects of protein oxidation; and redox proteomics analysis in human diseases. The chapters, which are written by experts in each topic, could be read as clear, comprehensive, and stand-alone critical reviews. However, the editors have chosen their topics well and assembled the chapters so they amount to more than the sum of their parts.

Part 1 maintains a balance between describing new methodology and the fundamental context in which the technology is applied. There is much of interest on the mass spectrometer, including MS approaches to oxidatively/nitrosatively modified proteins, glycosylation, multidimensional protein identification technology (MudPIT), protein thiols, nitrosothiols, and nitrosotyrosines.

Part 2 is not quite as comprehensive. However, the chapter by Aimee Lander et al. exploring the potential of thiol reactive lipid oxidation products in cell signalling is very thought-provoking. Chapter 15 (Thomas Nyström) explores how protein carbonylation relates to senescence in microbial systems and draws lessons for aging in higher organisms. Intriguingly, carbonylation seems to be kept low in all organisms at the reproductive life-cycle stage thus ensuring "fitness" of offspring.

Part 3 surveys applications of redox proteomics in studies of biomarkers of human disease, oxidized proteins in aging, Alzheimer's disease, vascular disease, diabetes, pre-eclampsia, and chronic airway diseases such as asthma. These studies make clear that redox proteomics will be a key arena for MS methods in future clinical research.

At 944 pages, this is a major book, which does credit to the editors. I think readers interested in mass spectrometry methods in proteomics will find much that is of interest here.

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